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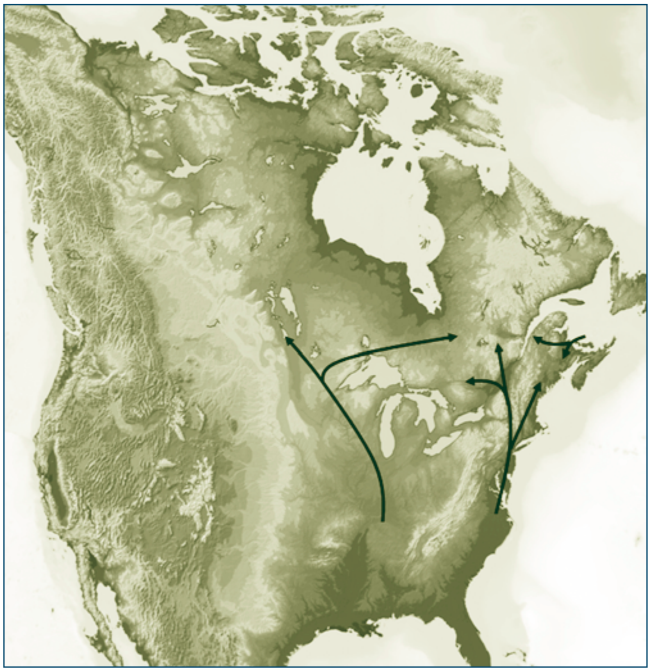
Uncovering the postglacial history of conifer populations

Roughly 18,000 years ago, a thick layer of ice covered all of Canada and the northern part of the United States. Most plant and animal species succumbed to the ice, and those that survived were confined to areas south of the ice front. As the climate warmed up, they began to spread northward, gradually building groups of populations that collectively form their present-day geographic range.

A team of Canadian Forest Service researchers and university colleagues embarked on a study aimed at tracing the path followed by tree species characteristic of Canadian forests, in particular jack pine and black spruce, from the start of deglaciation until the present time. Although this kind of portrait has traditionally been created by analyzing the fossil record (data on pollen, cones and needles), scientists can now reconstruct a species' history by comparing genetic differences between populations and making inferences about glacial refugia and postglacial colonization patterns.



Glacial populations and postglacial colonization routes for jack pine.

By examining the modern genetic structure of jack pine populations in the species' geographic range, the research team has identified three homogeneous groups of populations that are representative of genetically distinct glacial populations. The first group covers the western region extending from Lake Huron to the Yukon. The second one, representing the southeast region, consists mainly of populations located south of the St. Lawrence River in Quebec and in eastern Ontario. The third group is located in the Maritimes. Another distinct group, which is more genetically diverse, can be delineated in central Quebec, north of the St. Lawrence River. This region is believed to be a zone of contact between the migration fronts of the ancestral populations that colonized the other three zones.

Because of the marked differences found between the southeastern and western populations, it appears that a glacial jack pine population existed

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west of the Appalachians in the United States that was genetically distinct from another one located east of this mountain range. When the species began spreading northward toward Canada, glaciation likely persisted long enough in the northern part of the Appalachians to prevent the exchange of genetic material between the two populations. A similar pattern has been identified for black spruce east of the Rockies. Given the distinct genetic composition of the jack pine populations in the Maritimes, a third glacial population likely existed on the continental shelf of eastern Canada, which was not covered with ice at the time.


Jack pine stand.
Photo : RNCan


Black spruce stand.
Photo : RNCan

This hypothesis, which has also been put forward by botanists and entomologists, would help to explain the present-day distribution of boreal and arctic species in northeastern Nova Scotia, for example.

Sustainable use of the genetic resources of our forests can only be achieved by learning more about the origins and extent of this genetic diversity and its spatial organization. With a view to conserve biodiversity, jack pine and black spruce populations should be protected in all three regions because they likely came from distinct glacial populations. This kind of information can be used to identify potential threats to forest genetic resources from forestry practices and climate change. For example, the present-day jack pine populations derived from the glacial populations that were located on the unglaciated continental shelf of Canada or east of the Appalachians in the United States are probably better adapted to maritime conditions, which is why there should be no movement of seed sources between the Maritimes and the regions west of the province of Quebec.

Phylogeography

The science that seeks to reconstruct the history of living species based on the geographic distribution of their genetic variation, as we have done in this study, is called **phylogeography**. By comparing the genetic differences between populations for several species, scientists can make inferences about glacial refugia and postglacial colonization patterns.

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